

FIGURE 1

1 AGCTCCAGCCTAGGCGTTCTACCTGGAAGAAATGCAGGGGCCAGTACCTAGGACTGAGGA 60
 61 AGATGGCTGACATCCAGAACATTTTCGCTGGACAGCCAGGAGCGTAGGGCTGTGGCAG 120
 121 TGGCTGTGATCTTTGCCCTCAATCTTCCCTGTTGGGCAATGGTGGCAATGGGCTGGTGTGG 180
 181 CTGTGCTACTGCAGCCCTGGCCCAAGTGCCCTGGCAGAGCCAAAGCAGTACCACAGATCTCT 240
 241 TCATCCCTCAACTTGGCCGTGGCCGACCTTTGCTTCAATCCTGTGCTGCGTGCCCTTCCAGG 300
 301 CAGCCATCTACACACTGGATGCCCTGGCTCTTTGGGCTTTCTGTGCAAGACGGTACATC 360
 361 TGTCACTACCTACCAATGTAATGCCAGCAGCTTCACTTGGCGGCGTCTCCCTGGACA 420
 421 GTACCTGGCTGTGGCGCACCCACTGGCTCCAGAGCCCTGCGCACCCCGCGCAACGCGC 480
 481 GCGCGCCGTGGGCTCGTGTGGCTGCTGGCGGCTCTCTTTCCGCGCCCTACCTAAGCT 540
 541 ATTACGGCACGGTGCGCTACGGCGGCTCGAGCTCTGCGTGCCCGCTTGGGAGGACGCGC 600
 601 GGCGCGCGCGTGGACGTGGCCACCTTCGCCCGGGCTACCTGCTGCCGTGCCGTGGCGG 660
 661 TGAGCCCTGGCTACGGACGACGACGCGGACCGCGCGGGGACGCGCCATGCTGGCAG 720
 721 CGCGGCGAGCAGGCGCGCAGACGGGCGACCGCGCGGGGACGCGCCATGCTCTGCTCTGGT 780
 781 TGGCCGCGCTACGCGCTTTGCTGGGCGCCGACCAACGCGCTCATCTCTGCTCTGCTCTCG 840
 841 ACGCGCGCTTCGCTTACGCGCGCCACCTACGCTGTGCGCTGGCTCGCGCCACTTCCGCG 900
 901 CCTACGCCCAACTCTGCTTAACCCGCTCGCTTACCTGCTCGCTCGCGCCACTTCCGCG 960
 961 CGCGCTTCCGCGCGCTGTGGCCCTGCGGCGCTCGCGCCACCGCCACCAACCGCGCTC 1020
 1021 ATCGAGCCCTCCGTCTGTCCAGCCGGCGTCTTCGGGCGCCCGCGGTATCCCGCGGACG 1080
 1081 CCAGGCTCGTGGTGGAGTATGGAGCCAGAGGGATGCTCTGCGTGGTGGTGGAGAGA 1140
 1141 CTAGACTAACCTGTCCCCCAGGGACCTCAATAACCTGCCCGCTTGGACTCTGACGTC 1200
 1201 TGTCAGAATGCCACCAAGGAACATCTAGGGAACGGCAGTCTCGCCAGGCTCCACCAAAA 1260
 1261 GCAGAAGCAAGTTGCAGGG 1280

FIGURE 2

20	V	A	F	A	L	R	R	Y	R	V	A	V	Y	A	A	H	A	T
40	A	L	L	Q	H	D	A	S	A	V	G	A	W	L	R	A	D	E
60	V	V	D	F	V	L	N	L	D	A	A	L	F	C	F	R	G	G
80	A	L	T	P	T	S	R	Y	E	V	P	M	C	H	H	P	G	
100	G	G	T	V	K	V	P	P	W	P	G	A	L	S	R	H	Y	G
120	V	N	S	C	C	A	T	A	A	L	V	R	I	A	S	H	G	R
140	S	G	S	C	V	A	R	S	P	L	A	G	L	L	A	R	A	L
160	G	V	P	L	F	L	L	F	V	Y	A	A	A	R	L	H	P	A
180	P	M	E	I	A	T	A	L	C	G	W	R	H	C	S	R	G	D
200	S	G	Q	F	G	F	R	A	L	A	L	G	H	A	Y	R	S	G
220	D	L	W	C	F	S	S	A	E	A	F	T	P	Y	V	R	S	R
240	L	L	A	L	L	S	R	L	L	F	C	A	G	T	L	G	A	P
260	S	F	S	D	W	A	L	L	A	T	L	R	W	A	P	C	P	E
280	I	I	P	A	A	Y	P	W	G	A	T	R	C	P	N	P	Q	M
300	N	L	G	V	D	M	H	V	Y	V	R	R	L	S	L	W	V	S
320	Q	A	P	A	L	T	R	L	R	D	G	A	A	F	C	L	R	W
340	I	F	Q	L	T	L	V	G	V	L	Y	E	Y	A	S	R	R	G
360	D	I	L	N	Y	Y	A	V	T	A	A	A	L	F	N	R	L	R
370	A	V	L	L	I	I	L	A	G	R	L	A	A	R	A	F	A	P
	M	P	V	I	A	L	Y	A	Y	R	S	A	A	G	Y	R	R	R

[illegible]

FIGURE 4

1	20	P
21	40	T M P
41	60	V I T
61	80	L Y A
81	100	Y R S
101	120	A A G
121	140	Y R R
141	160	A A G
161	180	Y R R
181	200	A A G
201	220	Y R R
221	240	A A G
241	260	Y R R
261	280	A A G
281	300	Y R R
301	320	A A G
321	340	Y R R
341	360	A A G
361	380	Y R R
381	400	A A G
401	420	Y R R
421	440	A A G

P T M P V I T L Y A Y R S A A G Y R R G G
 Q R E V A F A L R R Y R V A V Y A A L S G
 F T G A L L Q H D A S A V G A W L R A P H
 S A D V V D F V V N L D A A L F C F R R V
 T Q S A L T P A S R Y E V P M C H H R A P
 P G P G G T V K V P P W P G A L S R A D G
 S R C V N S C C A T A A L V R I A S R G E
 P S R S G G C V A R S P L A G L L A H P R
 P R P G V P L L L L F V Y A A A R L R C P
 P V L P T E I A T A L C G W R H C A R G E
 S G S S G Q F G F R A L A L G H A Y R P P
 L G A D L W C F S S A E A F T P Y V R P G
 L V P L L A L L S R L L F R A G T L G G Q
 A Q I S F S D W A L L A T L R W A P C S G E
 L T R I I P A A Y P W G A T R C P N P S G P
 T Q L N L G V D M H V Y V R R L S L W A G G
 M G C Q A P A L T R L R D G A A F C L P A R
 A P S A F Q L T L V G V L Y E Y A S R R L A
 S T G D V L N Y Y A V T A A A L F N R V L A
 H R G A V L L I I L A G R L A A R A F R R E

hGALR3	M A D A Q N I S L D S P G	13
rGALR3	M A D I Q N I S L D S P G	13
rGALR1	M E L A P V N L S E G N G S D P E P P A E P R P L		25
hGALR3	S V G A V A V P V V F A L I F L L G T V G N	35
rGALR3	S V G A V A V P V I F A L I F L L G M V G N	35
rGALR1	F G I G V E N F I T L V V F F G L I F A M G V L G N		50
hGALR3	G L V L A V L L Q P G P S A W Q E P G S T T D L F		60
rGALR3	G L V L A V L L Q P G P S A W Q E P S S T T D L F		60
rGALR1	S L V I T V L A R S K P G . . . K P R S T T N L F		72
hGALR3	I L N L A V A D L C F I L C C V P P F Q A T I Y T L		85
rGALR3	I L N L A V A D L C F I L C C V P P F Q A I Y T L		85
rGALR1	I L N L S I A D L A Y L L F C I P F Q A T V Y A L		97

	III																									
hGALR3	D	A	W	L	F	G	A	L	V	C	K	A	V	H	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR3	D	A	W	L	F	G	A	F	V	C	K	T	V	H	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR1	P	T	W	V	L	G	A	F	I	C	K	F	I	H	Y	F	F	T	V	S	M	L	V	S	I	122
hGALR3	F	T	L	A	A	V	S	V	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T	135
rGALR3	F	T	L	A	A	V	S	L	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T	135
rGALR1	F	T	L	A	A	M	S	V	D	R	Y	V	A	I	V	H	S	R	R	S	S	L	R	V	147	
hGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y	160
rGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y	160
rGALR1	S	R	N	A	L	L	G	V	G	F	I	W	A	L	S	I	A	M	A	S	P	.	V	A	Y	171
hGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R	182
rGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R	182
rGALR1	Y	Q	R	L	F	H	R	D	S	N	Q	T	F	F	C	W	E	H	P	N	Q	L	H	K	K	196

FIGURE 5C

hGALR3 rGALR3 rGALR1	V														207 207 221										
	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	S	L	A	Y	G	R	T	
	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	S	L	A	Y	G	R	T	
hGALR3 rGALR3 rGALR1	A	Y	V	V	C	T	F	V	F	G	Y	L	L	P	L	L	I	C	F	Y	A	K	V		
	VI														232 232 242										
	L	R	F	L	W	A	A	V	G	P	A	G	A	A	A	A	E	A	R	R	A	T	G	R	
hGALR3 rGALR3 rGALR1	L	C	F	L	W	A	A	V	G	P	A	G	A	A	A	E	A	R	R	A	T	G	R		
	L	N	H	L	H	K	K	L	K	N	M	S	K	K	S	E	A	S	K	.	.	.	K		
	VI														257 257 267										
hGALR3 rGALR3 rGALR1	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C
	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C
	T	A	Q	T	V	L	V	V	V	V	V	F	G	I	S	W	L	P	H	H	V	I	H	L	W
hGALR3 rGALR3 rGALR1	VII														282 282 292										
	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A
	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A
hGALR3 rGALR3 rGALR1	A	E	F	G	A	F	P	L	T	P	A	S	F	F	F	R	I	T	A	H	C	L	A	Y	S

FIGURE 5D

hGALR3	N	S	C	L	N	P	L	V	Y	A	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR3	N	S	C	L	N	P	L	V	Y	S	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR1	N	S	S	V	N	P	I	I	Y	A	F	L	S	E	N	F	R	K	A	Y	K	Q	V	F	K	317
hGALR3	C	G	R	R	R	.	.	.	R	H	R	A	R	R	A	L	R	R	V	R	P	A	S	S	G	329
rGALR3	C	G	R	R	R	H	R	H	H	R	A	H	R	A	L	R	R	V	Q	P	A	S	S	G	332	
rGALR1	C	R	V	C	N	E	S	P	H	G	D	A	K	E	K	N	R	I	D	T	P	P	S	T	N	342
hGALR3	P	P	G	C	P	G	D	A	R	P	S	G	R	L	L	A	G	G	Q	G	P	E	P	R	354	
rGALR3	P	A	G	Y	P	G	D	A	R	P	R	G	W	S	M	E	P	R	350		
rGALR1	C	T	H	V	346	
hGALR3	E	G	P	V	H	G	G	E	A	A	R	G	P	E	.	.	.	368		
rGALR3	G	D	A	L	R	G	G	E	T	R	L	T	L	S	P	R	G	P	Q	370		

FIG. 6A

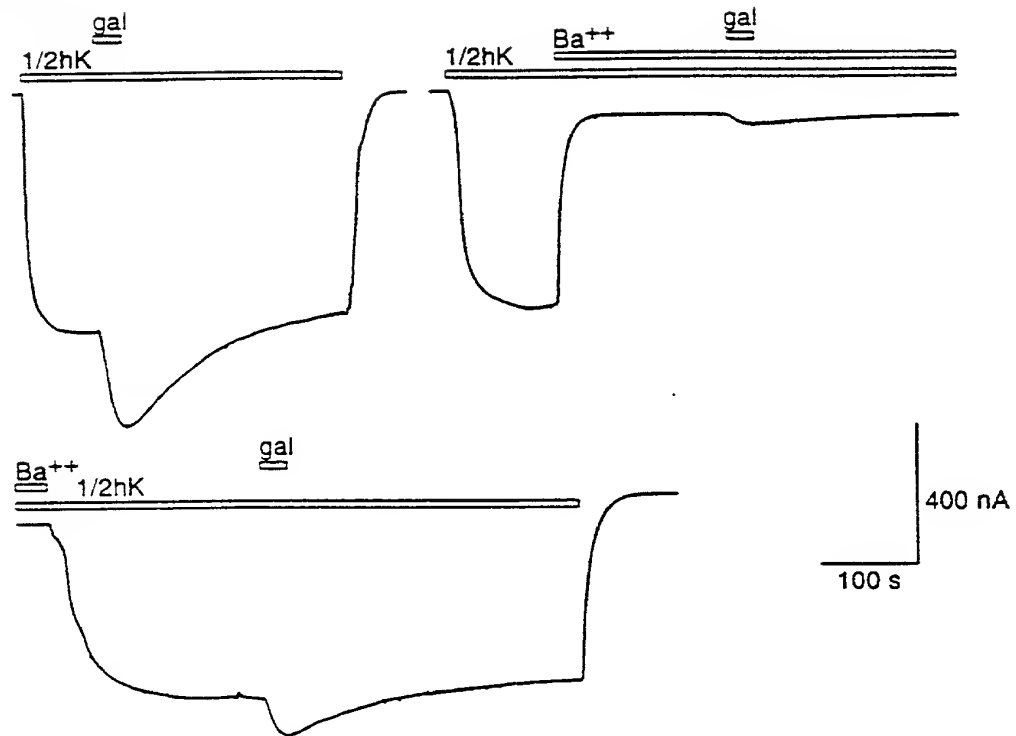


FIG. 6B

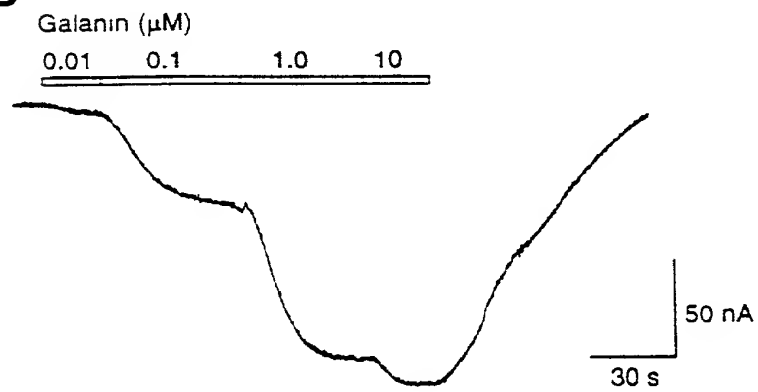
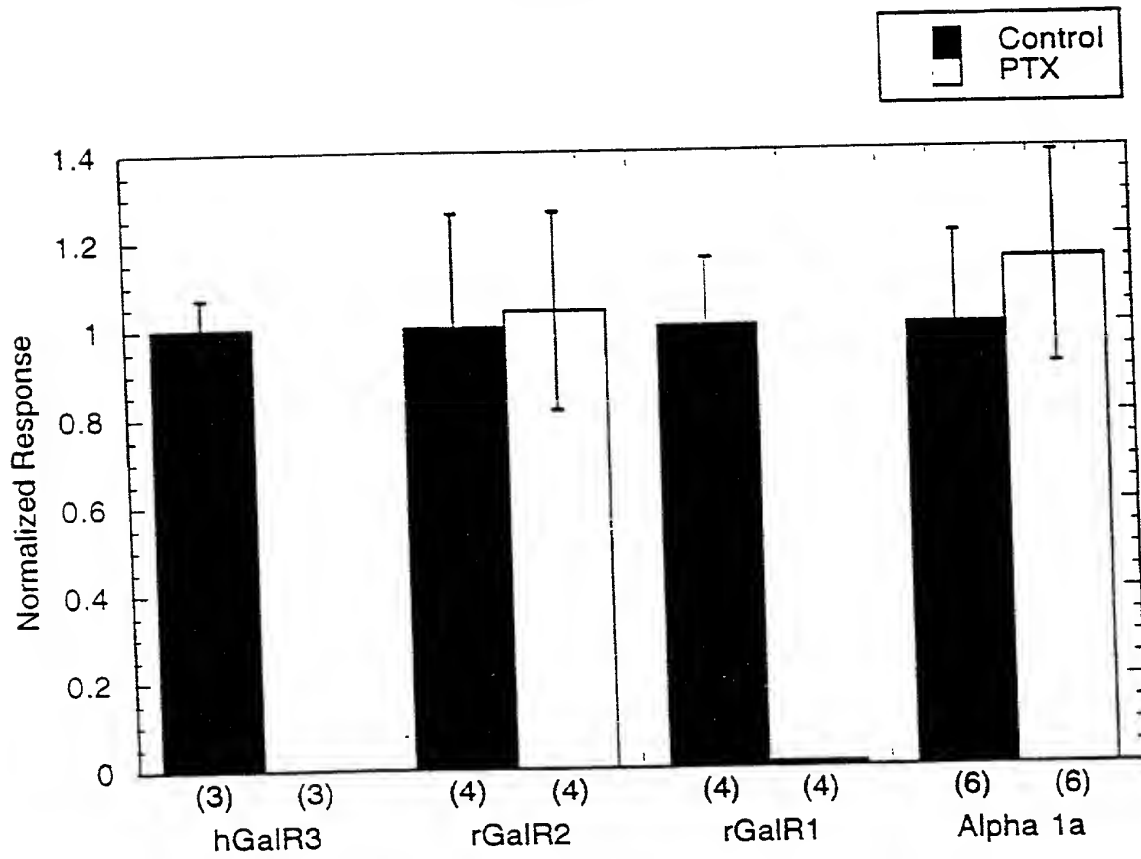


FIG. 7



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FIG. 8A

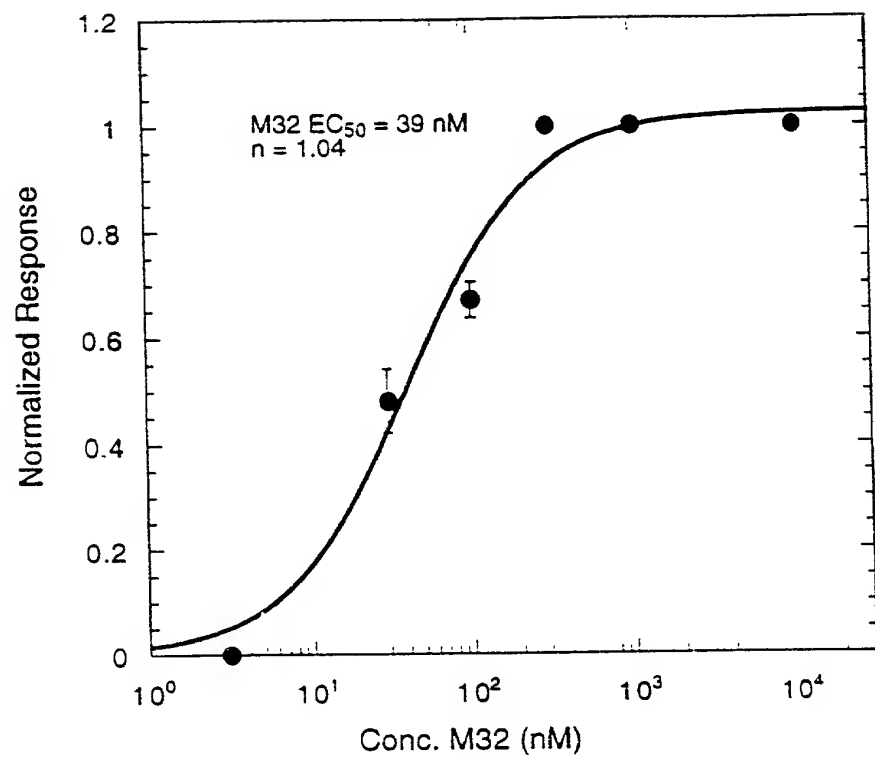


FIG. 8B

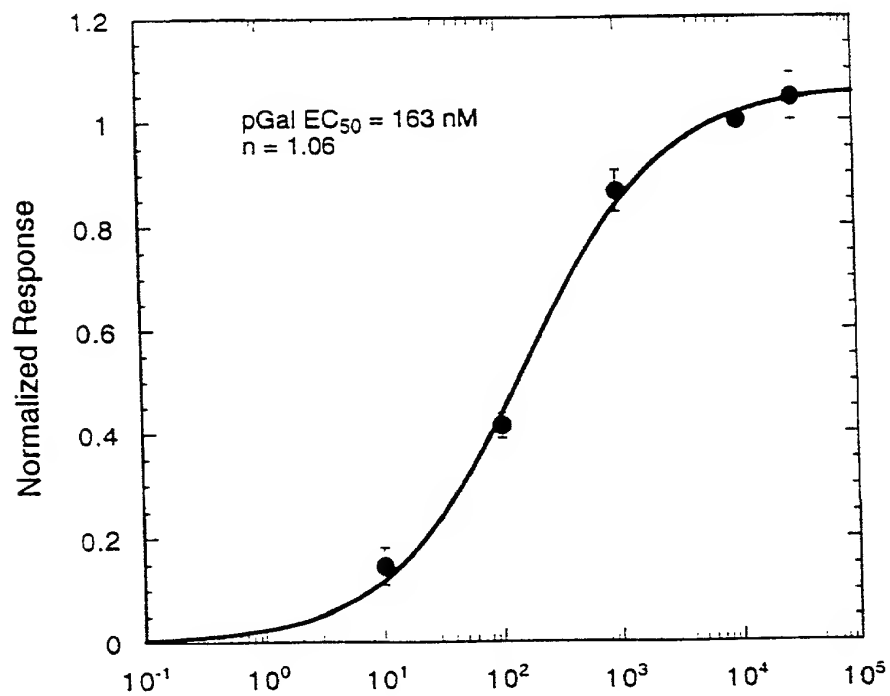


FIG. 8C

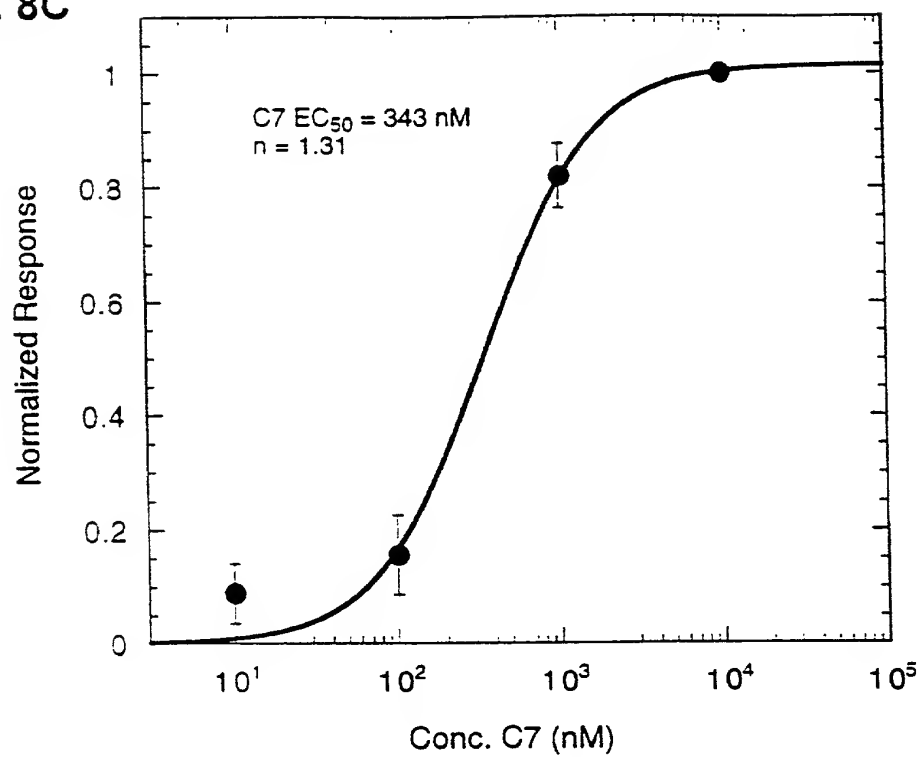


FIG. 8D

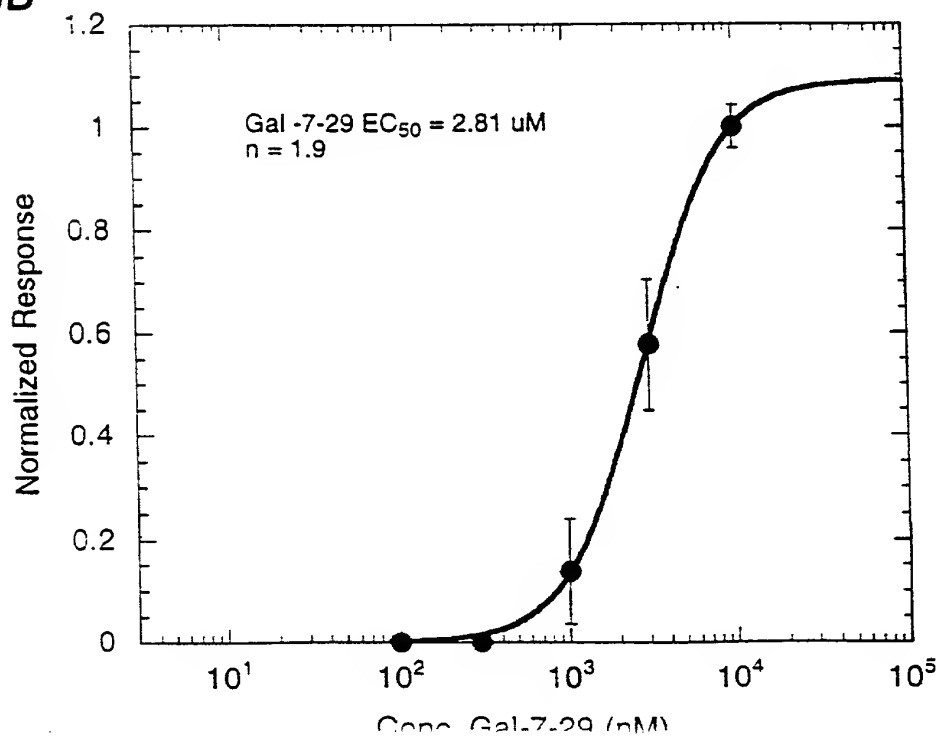


FIG. 8E

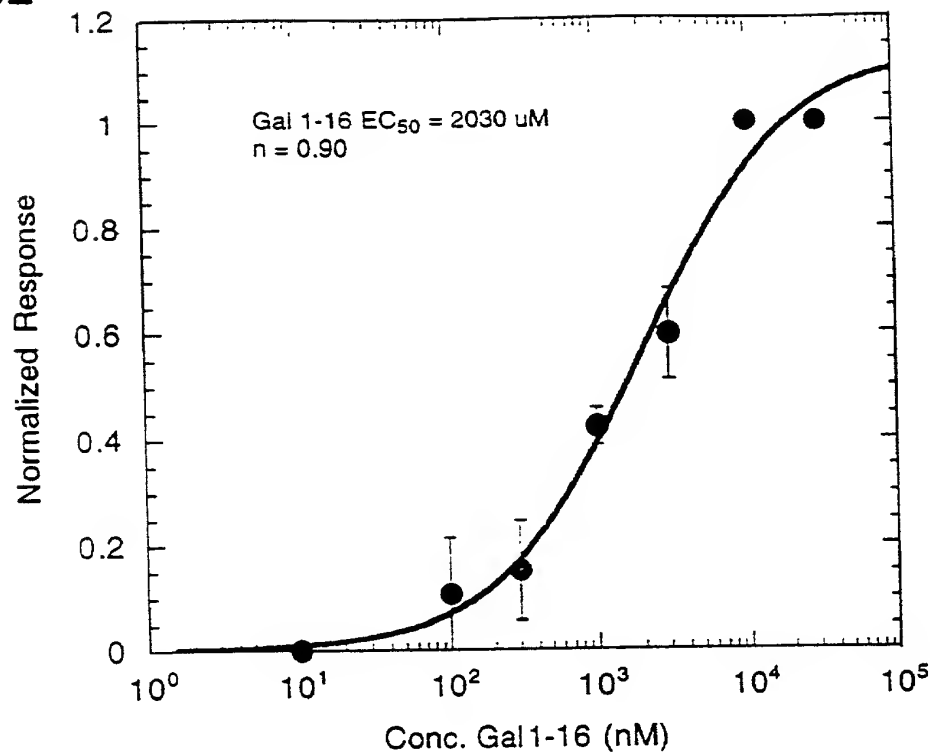


FIG. 8F

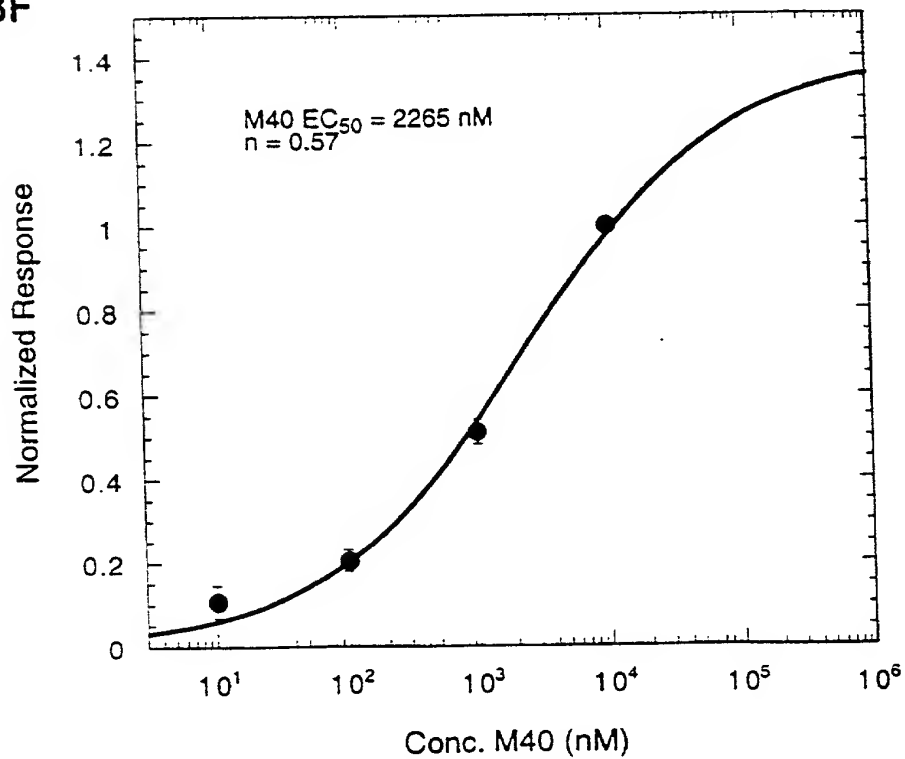


FIG. 9A

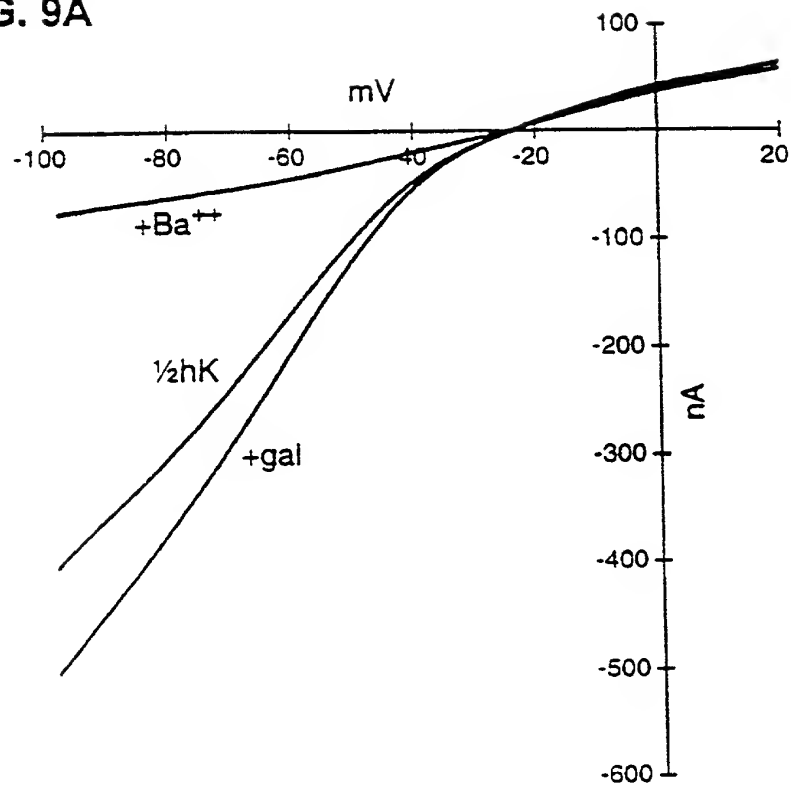


FIG. 9B

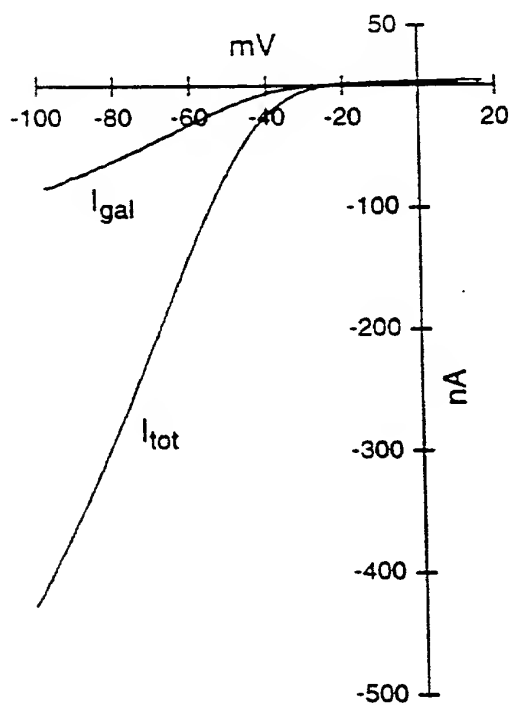


FIG. 10

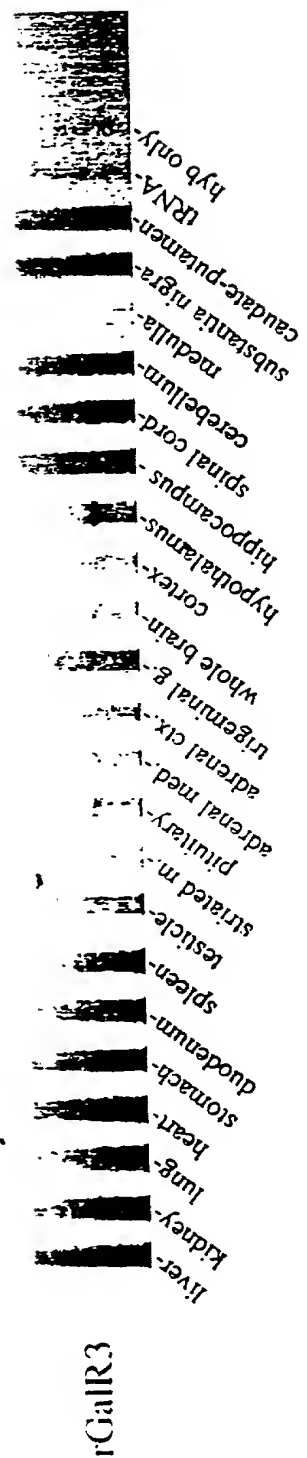


FIG. 11

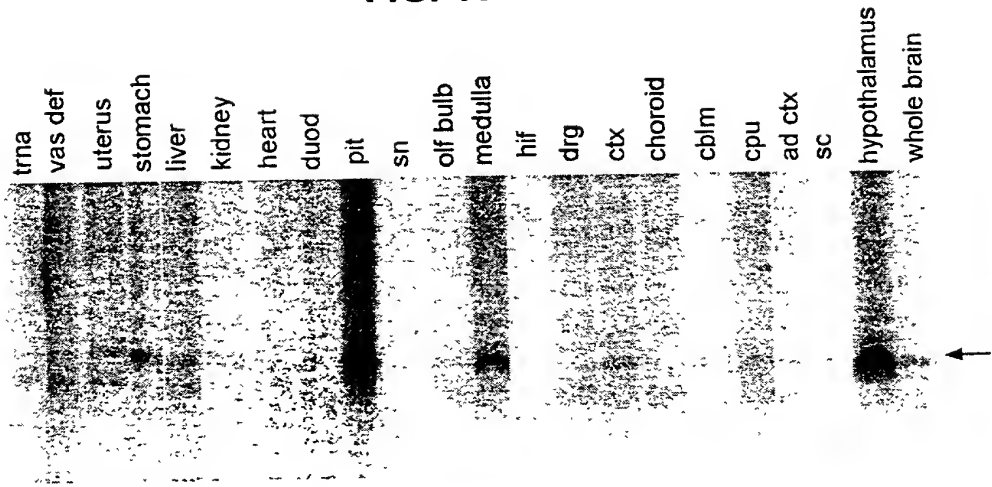


FIG. 12

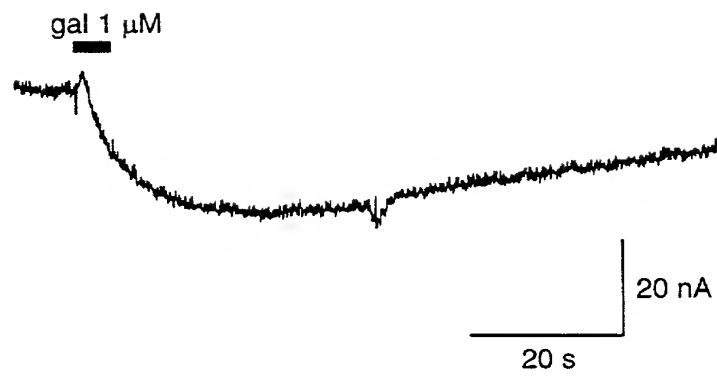


FIG. 13A

hGALR3-LM #228 **+/- Pertussis Toxin**

Guanine nucleotide effects

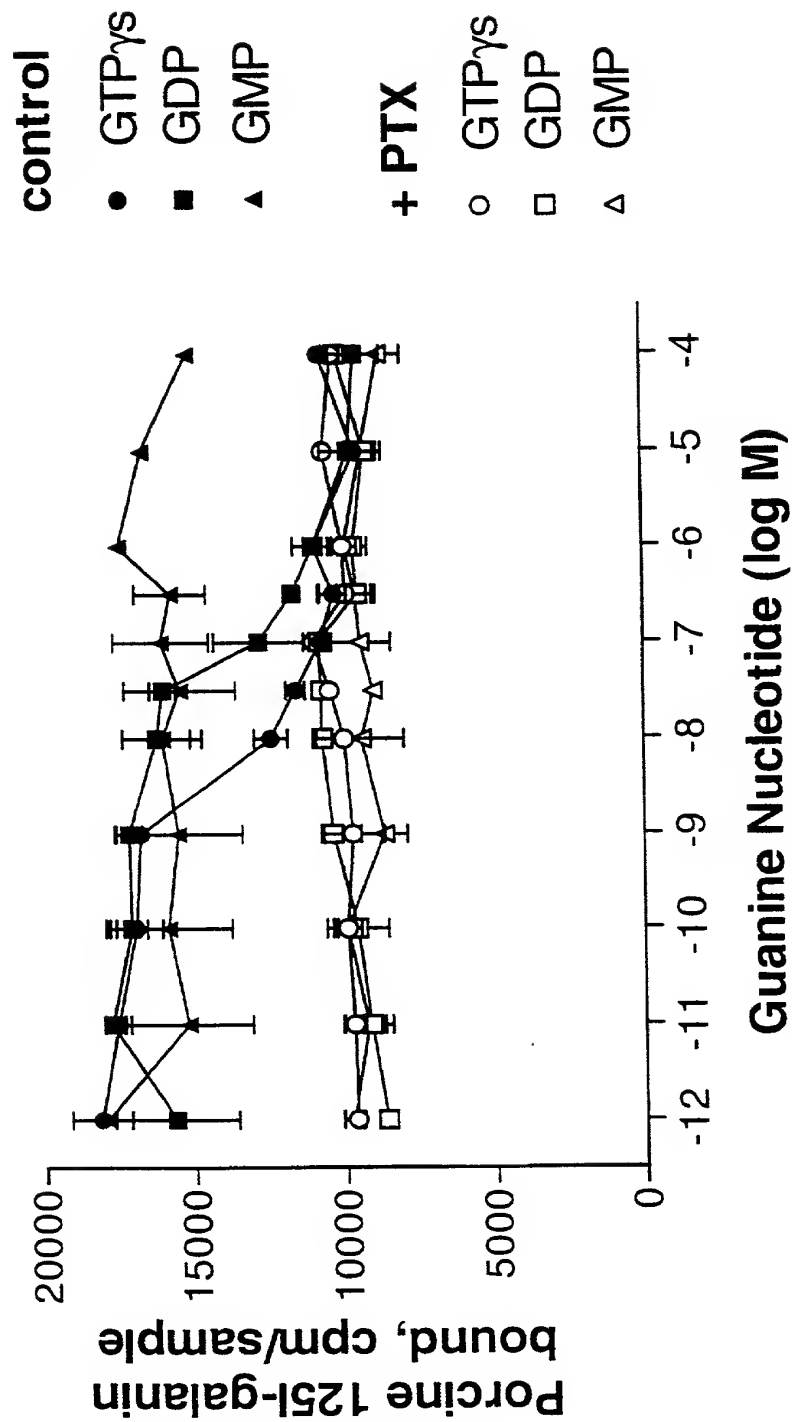


FIG. 13B
Nonspecific Binding
with 1 μ M p galanin

